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Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.**Nagase T, Ishikawa K, Suyama M, Kikuno R, Hirose M, Miyajima N, Tanaka A, Kotani H, Nomura N, Ohara O**

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Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.

As a part of our cDNA project for deducing the coding sequence of unidentified human genes, we newly determined the sequences of 100 cDNA clones from a set of size-fractionated human brain cDNA libraries, and predicted the coding sequences of the corresponding genes, named KIAA0919 to KIAA1018. The sequencing of these clones revealed that the average sizes of the inserts and corresponding open reading frames were 4.9 kb and 2.6 kb (882 amino acid residues), respectively. A computer search of the sequences against the public databases indicated that predicted coding sequences of 87 genes contained sequences similar to known genes, 53% of which (46 genes) were categorized as proteins relating to cell signaling/communication, cell structure/motility and nucleic acid management. The chromosomal locations of the genes were determined by using human-rodent hybrid panels unless their mapping data were already available in the public databases. The expression profiles of all the genes among 10 human tissues, 8 brain regions (amygdala, corpus callosum, cerebellum, caudate nucleus, hippocampus, substantia nigra, subthalamic nucleus, and thalamus), spinal cord, fetal brain and fetal liver were also examined by reverse transcription-coupled polymerase chain reaction, products of which were quantified by enzyme-linked immunosorbent assay.

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